

Figure 1

```

      1      10      20      30
      *      *      *      *
G AATTCGCTA CTA CTCAACA ATG AAG ATG CTT TAC GCT ATC GCT
      Met Lys Met Leu Tyr Ala Ile Ala

      40      50      60      70
      *      *      *      *
ATA ATG TTT CTC CTG GTA TCA TTA TGC AGC GCA AGA ACA GTG
Ile Met Phe Leu Leu Val Ser Leu Cys Ser Ala Arg Thr Val

      80      90      100      110      120
      *      *      *      *      *
AGG AAG GCA TAC CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC
Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp

      130      140      150      160
      *      *      *      *
GAC TGT GGA ACT CAG AAG CCA TGC GAG GCC AAG TGC AAT GAG
Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu

      170      180      190      200
      *      *      *      *
GAA CCC CCT GAG GAG GAA GAT CCG ATA TGC CGC TCA CGT GGT
Glu Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly

      210      220      230      240
      *      *      *      *
TGT TTA TTA CCT CCT GCT TGC GTA TGC AAA GAC GGA TTC TAC
Cys Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr

      250      260      270      280
      *      *      *      *
AGA GAC ACG GTG ATC GGC GAC TGT GTT AGG GAA GAA GAA TGC
Arg Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu Glu Cys

      290      300      310      320      330
      *      *      *      *      *
GAC CAA CAT GAG ATT ATA CAT GTC TGA ACGAGAAAGC AACAATAACC
Asp Gln His Glu Ile Ile His Val

      340      350      360      370      380
      *      *      *      *      *
AAAGGTTCCA ACTCTCGCTC TGCAAAATCG CTAGTTGGAT GTCTCTTTTG

      390      400      410      420      430
      *      *      *      *      *
CGTCCGAATA GTTTTAGTTG ATGTTAAGTA AGAACTCCTG CTGGAGAGAA

      440      450
      *      *
TAAAGCTTTC CAACTCC poly(A)

```

Figure 2

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Asp
 1 5 10

Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys Cys Asn Glu Glu
 15 20 25

Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg Ser Arg Gly Cys
 30 35 40

Leu Leu Pro Pro Ala Cys Val Cys Lys Asp Gly Phe Tyr Arg
 45 50 55

Asp Thr Val Ile Gly Asp Cys Val Arg Glu Glu Glu Cys Asp
 60 65 70

Gln His Glu Ile Ile His Val
 75

Figure 3

```

      1      10      20      30
      *      *      *      *
G AATTCGCTA CTAACA ATG AAG ATG CTT TAC GCT ATC GCT
  Met Lys Met Leu Tyr Ala Ile Ala

      40      50      60      70
      *      *      *      *
ATA ATG TTT CTC CTG GTG TCA TTA TGC AGC ACA AGA ACA GTG
Ile Met Phe Leu Leu Val Ser Leu Cys Ser Thr Arg Thr Val

      80      90      100      110      120
      *      *      *      *      *
AGG AAG GCA TAC CCG GAG TGT GGT GAG AAT GAA TGG CTC GAC
Arg Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp

      130      140      150      160
      *      *      *      *
GTC TGT GGA ACT AAG AAG CCA TGC GAG GCC AAG TGC AGT GAG
Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu

      170      180      190      200
      *      *      *      *
GAA GAG GAG GAA GAT CCG ATA TGC CGA TCA TTT TCT TGT CCG
Glu Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro

      210      220      230      240
      *      *      *      *
GGT CCC GCT GCT TGC GTA TGC GAA GAC GGA TTC TAC AGA GAC
Gly Pro Ala Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp

      250      260      270      280
      *      *      *      *
ACG GTG ATC GGC GAC TGT GTT AAG GAA GAA GAA TGC GAC CAA
Thr Val Ile Gly Asp Cys Val Lys Glu Glu Glu Cys Asp Gln

      290      300      310      320      330
      *      *      *      *      *
CAT GAG ATT ATT CAT GTC TGA ACGAGAGAGC AGTAATAACC
His Glu Ile Ile His Val

      340      350      360      370      380
      *      *      *      *      *
AAAGGTTCCA ACTTCGCTC TACAAAATCG CTAGTTGGAT TTCTCCTTG

      390      400      410      420      430
      *      *      *      *      *
CGTGCGAATA GTTTTAGTTG ATATTAAGTA AAACCTCCTG TTGAAGAGAA

      440
      *
TAAAGCTTTC CAACTTC poly(A)

```

Figure 4

Lys Ala Tyr Pro Glu Cys Gly Glu Asn Glu Trp Leu Asp Val
 1 5 10

Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys Cys Ser Glu Glu
 15 20 25

Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe Ser Cys Pro Gly
 30 35 40

Pro Ala Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg Asp Thr
 45 50 55

Val Ile Gly Asp Cys Val Lys Glu Glu Glu Cys Asp Gln His
 60 65 70

Glu Ile Ile His Val
 75

Trp Leu Asp Asp Cys Gly Thr Gln Lys Pro Cys Glu Ala Lys
15 20

Cys Asn Glu Glu Pro Pro Glu Glu Glu Asp Pro Ile Cys Arg
25 30 35

Ser Arg Gly Cys Leu Leu Pro Pro Ala Cys Val Cys Lys Asp
40 45 50

Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Arg Glu
55 60 65

Glu Glu Cys Asp Gln His Glu Ile Ile His Val
70 75

Trp Leu Asp Val Cys Gly Thr Lys Lys Pro Cys Glu Ala Lys
15 20

Cys Ser Glu Glu Glu Glu Asp Pro Ile Cys Arg Ser Phe
25 30 35

Ser Cys Pro Gly Pro Ala Ala Cys Val Cys Glu Asp Gly Phe
40 45 50

Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Lys Glu Glu Glu
55 60 65

Cys Asp Gln His Glu Ile Ile His Val
70 75

Figure 7A-1

1	10	20	30	40
*	*	*	*	*
<u>GAATTC</u> ACTA TTATCCAACA ATG GCG GTG CTT TAT TCA GTA GCA				
EcoRI Met Ala Val Leu Tyr Ser Val Ala				
50	60	70	80	
*	*	*	*	
ATA GCG TTA CTA CTG GTA TCA CAA TGC AGT GGG AAA CCG AAC				
Ile Ala Leu Leu Leu Val Ser Gln Cys Ser Gly Lys Pro Asn				
90	100	110	120	
*	*	*	*	
AAT GTG ATG ACT AAC GCT TGT GGT CTT AAT GAA TAT TTC GCT				
Asn Val Met Thr Asn Ala Cys Gly Leu Asn Glu Tyr Phe Ala				
130	140	150	160	170
*	*	*	*	*
GAG TGT GGC AAT ATG AAG GAA TGC GAG CAC AGA TGC AAT GAG				
Glu Cys Gly Asn Met Lys Glu Cys Glu His Arg Cys Asn Glu				
180	190	200	210	
*	*	*	*	
GAG GAA AAT GAG GAA AGG GAC GAG GAA AGA ATA ACG GCA TGC				
Glu Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile Thr Ala Cys				
220	230	240	250	
*	*	*	*	
CTC ATC CGT GTG TGT TTC CGT CCT GGT GCT TGC GTA TGC AAA				
Leu Ile Arg Val Cys Phe Arg Pro Gly Ala Cys Val Cys Lys				
260	270	280	290	
*	*	*	*	
GAC GGA TTC TAT AGA AAC AGA ACA GGC AGC TGT GTG GAA GAA				
Asp Gly Phe Tyr Arg Asn Arg Thr Gly Ser Cys Val Glu Glu				
300	310	320	330	
*	*	*	*	
GAT GAC TGC GAG TAC GAG AAT ATG GAG TTC ATT ACT TTT GCA				
Asp Asp Cys Glu Tyr Glu Asn Met Glu Phe Ile Thr Phe Ala				
340	350	360	370	380
*	*	*	*	*
CCA GAA GTA CCG ATA TGT GGT TCC AAC GAA AGG TAC TCC GAC				
Pro Glu Val Pro Ile Cys Gly Ser Asn Glu Arg Tyr Ser Asp				
390	400	410	420	
*	*	*	*	
TGC GGC AAT GAC AAA CAA TGC GAG CGC AAA TGC AAC GAG GAC				
Cys Gly Asn Asp Lys Gln Cys Glu Arg Lys Cys Asn Glu Asp				
430	440	450	460	
*	*	*	*	
GAT TAT GAG AAG GGA GAT GAG GCA TGC CGC TCA CAT GTT TGT				
Asp Tyr Glu Lys Gly Asp Glu Ala Cys Arg Ser His Val Cys				

Figure 7A-2

470 *	480 *	490 *	500 *
GAA CGT CCT GGT GCC TGT GTA TGC GAA GAC GGG TTC TAC AGA			
Glu Arg Pro Gly Ala Cys Val Cys Glu Asp Gly Phe Tyr Arg			
510 *	520 *	530 *	540 *
AAC AAA AAA GGT AGC TGT GTG GAA AGC GAT GAC TGC GAA TAC			
Asn Lys Lys Gly Ser Cys Val Glu Ser Asp Asp Cys Glu Tyr			
550 *	560 *	570 *	580 *
GAT AAT ATG GAT TTC ATC ACT TTT GCA CCA GAA ACC TCA CGA			
Asp Asn Met Asp Phe Ile Thr Phe Ala Pro Glu Thr Ser Arg			
600 *	610 *	620 *	630 *
TAA CCAAAGATGC TACCTCTCGT ACGCAACTCC GCTGATTGAGGTTGATTC			
650 *	660 *	670 *	680 *
ACTCCCTTGCATCTCAACATTTTTTTTGTGATGCTGTGCATCTGAGCTTAACCTG			
700 *	710 *		
ATAAAGCCTATGGTG poly(A)			

Figure 7B

```

1      10      20      30      40
*      *      *      *      *
GAATTC CGC ATG CGG ACG CTC TAC CTC ATT TCT ATC TGG TTG
EcoRI      Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu

50      60      70      80
*      *      *      *
TTC CTC ATC TCG CAA TGT AAT GGA AAA GCA TTC CCG AAA TGT
Phe Leu Ile Ser Gln Cys Asn Gly Lys Ala Phe Pro Lys Cys

90      100     110     120
*      *      *      *
GAC GTC AAT GAA AGA TTC GAG GTG TGT GGC AAT CTG AAG GAG
Asp Val Asn Glu Arg Phe Glu Val Cys Gly Asn Leu Lys Glu

130     140     150     160
*      *      *      *
TGC GAG CTC AAG TGC GAT GAG GAC CCT AAG ATA TGC TCT CGT
Cys Glu Leu Lys Cys Asp Glu Asp Pro Lys Ile Cys Ser Arg

170     180     190     200     210
*      *      *      *      *
GCA TGT ATT CGT CCC CCT GCT TGC GTA TGC GAT GAC GGA TTC
Ala Cys Ile Arg Pro Pro Ala Cys Val Cys Asp Asp Gly Phe

220     230     240     250
*      *      *      *
TAC AGA GAC AAA TAT GGC TTC TGT GTT GAA GAA GAC GAA TGT
Tyr Arg Asp Lys Tyr Gly Phe Cys Val Glu Glu Asp Glu Cys

260     270     280     290
*      *      *      *
AAC GAT ATG GAG ATT ATT ACT TTT CCA CCA GAA ACC AAA TGA
Asn Asp Met Glu Ile Ile Thr Phe Pro Pro Glu Thr Lys

300     310     320     330     340
*      *      *      *      *
TGACCGAAGC TTCCACCTTT CTATACATAT CTTCACTGCTTGACAGGCTTCT

350     360     370     380     390     400
*      *      *      *      *
CGACAATTTAGAAGTTCTGCTTGACTTTGTCTATTTGAAATTGTTTCACTAATG

410     420
*      *
GGGGAAGTAAAGCATTTTCACGAC poly(A)

```

Figure 7C

```

1      10      20      30      40
*      *      *      *      *
GAATTCCGCT ACATTTTCAA CA ATG TCG ACG CTT TAT GTT ATC
EcoRI                      Met Ser Thr Leu Tyr Val Ile

      50      60      70      80
      *      *      *      *
GCA ATA TGT TTG CTG CTT GTT TCG CAA TGC AAT GGA AGA ACG
Ala Ile Cys Leu Leu Leu Val Ser Gln Cys Asn Gly Arg Thr

      90      100      110      120
      *      *      *      *
GTG AAG AAG TGT GGC AAG AAT GAA AGA TAC GAC GAC TGT GGC
Val Lys Lys Cys Gly Lys Asn Glu Arg Tyr Asp Asp Cys Gly

130      140      150      160
*      *      *      *
AAT GCA AAG GAC TGC GAG ACC AAG TGC GGT GAA GAG GAA AAG
Asn Ala Lys Asp Cys Glu Thr Lys Cys Gly Glu Glu Glu Lys

170      180      190      200      210
*      *      *      *      *
GTG TGC CGT TCG CGT GAG TGT ACT AGT CCT GGT GCC TGC GTA
Val Cys Arg Ser Arg Glu Cys Thr Ser Pro Gly Ala Cys Val

      220      230      240      250
      *      *      *      *
TGC GAA CAA GGA TTC TAC AGA GAT CCG GCT GGC GAC TGT GTC
Cys Glu Gln Gly Phe Tyr Arg Asp Pro Ala Gly Asp Cys Val

      260      270      280      290
      *      *      *      *
ACT GAT GAA GAA TGT GAT GAA TGG AAC AAT ATG GAG ATC ATT
Thr Asp Glu Glu Cys Asp Glu Trp Asn Asn Met Glu Ile Ile

      300      310      320      330      340
      *      *      *      *      *
ACT ATG CCA AAA CAG TAG TGCGAAGTTC CCTTCTTTCT CCAAATCTG
Thr Met Pro Lys Gln

      350      360      370      380      390
      *      *      *      *      *
C TCCGTGCTCAATTATCACACACCTCCACTAGTTAAGATTGACTGACTCTCTTG

      400      410      420      430      440      450
      *      *      *      *      *      *
CATTTAGTATTTTCGCTTGACTCTGTGCATTTAAGCATGAGATACTACTAGGGA

      460      470
      *      *
GAATAAAAATTACTA ACTAC poly(A)

```

Figure 7D

```

1      10      20      30      40
*      *      *      *      *
GAATTCGG AAA TGT CCT ACC GAT GAA TGG TTC GAT TGG TGT
EcoRI      Lys Cys Pro Thr Asp Glu Trp Phe Asp Trp Cys

50      60      70      80
*      *      *      *
GGA ACT TAC AAG CAT TGC GAA CTC AAG TGC GAT AGG GAG CTA
Gly Thr Tyr Lys His Cys Glu Leu Lys Cys Asp Arg Glu Leu

90      100      110      120
*      *      *      *
ACT GAG AAA GAA GAG CAG GCA TGT CTC TCA CGT GTT TGT GAG
Thr Glu Lys Glu Glu Gln Ala Cys Leu Ser Arg Val Cys Glu

130      140      150      160
*      *      *      *
AAG TCC GCT TGC GTA TGC AAT GAC GGA TTA TAC AGA GAC AAG
Lys Ser Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Lys

170      180      190      200      210
*      *      *      *      *
TTT GGC AAC TGT GTT GAA AAA GAC GAA TGC AAC GAT ATG GAG
Phe Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu

220      230      240      250
*      *      *      *
ATT ATT ACT TTT GCA CCA GAA ACC AAA TAA TGGCCTAAGG TTCC
Ile Ile Thr Phe Ala Pro Glu Thr Lys

260      270      280      290      300
*      *      *      *      *
AAACCT TGCTACACAC CGTCAGTGCTTTACTGTTTCCTCTACGTGTTAGTAGT

310      320      330      340      350      360
*      *      *      *      *      *
TTTGCTTGACTCTGTGTATTTAAGCATTGTCTACTAATGGGCAAAGTAAAGCATT

370      380      390
*      *      *
GTAAGGACATAATAATGAGTAAACCTTCTGATTT poly(A)

```

Figure 7E-1

1	10	20	30	40
*	*	*	*	*
<u>GAATTC</u> CGGG CGGCAGAAAG ATG CGA ATG CTC TAC CTT GTT CCT				
EcoRI Met Arg Met Leu Tyr Leu Val Pro				
50	60	70	80	
*	*	*	*	
ATC TGG TTG CTG CTC ATT TCG CTA TGC AGT GGA AAA GCT GCG				
Ile Trp Leu Leu Leu Ile Ser Leu Cys Ser Gly Lys Ala Ala				
90	100	110	120	
*	*	*	*	
AAG AAA TGT GGT CTC AAT GAA AGG CTG GAC TGT GGC AAT CTG				
Lys Lys Cys Gly Leu Asn Glu Arg Leu Asp Cys Gly Asn Leu				
130	140	150	160	170
*	*	*	*	*
AAG CAA TGC GAG CCC AAG TGC AGC GAC TTG GAA AGT GAG GAG				
Lys Gln Cys Glu Pro Lys Cys Ser Asp Leu Glu Ser Glu Glu				
180	190	200	210	
*	*	*	*	
TAT GAG GAG GAA GAT GAG TCG AAA TGT CGA TCA CGT GAA TGT				
Tyr Glu Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys				
220	230	240	250	
*	*	*	*	
TCT CGT CGT GTT TGT GTA TGC GAT GAA GGA TTC TAC AGA AAC				
Ser Arg Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn				
260	270	280	290	
*	*	*	*	
AAG AAG GGC AAG TGT GTT GCA AAA GAT GTT TGC GAG GAC GAC				
Lys Lys Gly Lys Cys Val Ala Lys Asp Val Cys Glu Asp Asp				
300	310	320	330	
*	*	*	*	
AAT ATG GAG ATT ATC ACT TTT CCA CCA GAA GAC GAA TGT GGT				
Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Glu Cys Gly				
340	350	360	370	380
*	*	*	*	*
CCC GAT GAA TGG TTC GAC TAC TGT GGA AAT TAT AAG AAG TGC				
Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr Lys Lys Cys				
390	400	410	420	
*	*	*	*	
GAA CGC AAG TGC AGT GAG GAG ACA AGT GAG AAA AAT GAG GAG				
Glu Arg Lys Cys Ser Glu Glu Thr Ser Glu Lys Asn Glu Glu				
430	440	450	460	
*	*	*	*	
GCA TGC CTC TCT CGT GCT TGT ACT GGT CGT GCT TGC GTA TGC				
Ala Cys Leu Ser Arg Ala Cys Thr Gly Arg Ala Cys Val Cys				

Figure 7E-2

470		480		490		500
*		*		*		*
AAA GAC GGA TTG TAC AGA GAC GAC TTT GGC AAC TGT GTT CCA						
Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn Cys Val Pro						
510		520		530		540
*		*		*		*
CAT GAC GAA TGC AAC GAT ATG GAG ATC ATC ACT TTT CCA CCG						
His Asp Glu Cys Asn Asp Met Glu Ile Ile Thr Phe Pro Pro						
550		560		570		580
*		*		*		*
GAA ACC AAA CAT TGA CCAGAGGCTC CAACTCTCGC TACACAACGT CA						
Glu Thr Lys His						
600		610		620		630
*		*		*		*
GGGCTAGAATGGCCCCTCTGCGAGTTAGTAGTTTTGCTTGACTCTGCTTATTGA						
660		670		680		
*		*		*		
GCACTTTCTATTGATGGCGAAAATAAAGCATTTAAAC poly(A)						

Figure 7F

```

      1          10          20          30          40
      *          *          *          *          *
      GAATTCCGCG CACCTGAGAG GTGAGCTACG CAAGTCTTCG CTGGTACA
      EcoRI

50          60          70          80          90
*          *          *          *          *
ATG ATC CGA AAG CTC GTT CTG CTG ACT GCT ATC GTC ACG GTG
Met Ile Arg Lys Leu Val Leu Leu Thr Ala Ile Val Thr Val

      100          110          120          130
      *          *          *          *
GTG CTA AGT GCG AAG ACC TGT GGA CCA AAC GAG GAG TAC ACT
Val Leu Ser Ala Lys Thr Cys Gly Pro Asn Glu Glu Tyr Thr

      140          150          160          170
      *          *          *          *
GAA TGC GGG ACG CCA TGC GAG CCG AAG TGC AAT GAA CCG ATG
Glu Cys Gly Thr Pro Cys Glu Pro Lys Cys Asn Glu Pro Met

      180          190          200          210
      *          *          *          *
CCA GAC ATC TGT ACT CTG AAC TGC ATC GTG AAC GTG TGT CAG
Pro Asp Ile Cys Thr Leu Asn Cys Ile Val Asn Val Cys Gln

      220          230          240          250
      *          *          *          *
TGC AAA CCC GGC TTC AAG CGC GGA CCG AAA GGA TGC GTC GCC
Cys Lys Pro Gly Phe Lys Arg Gly Pro Lys Gly Cys Val Ala

260          270          280          290          300
*          *          *          *          *
CCC GGA CCA GGC TGT AAA TAG TTCTCCACCT GCCCTTTCGT TGGAA
Pro Gly Pro Gly Cys Lys

      310          320          330          340
      *          *          *          *
CAAAT GGCTGTCTTTTTTACATTCTGAATCAATAAAGCCGAACGGT poly(A)

```

Figure 8A

```

      1      10      20      30      40
      *      *      *      *      *
  AAGCTT TGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT
HindIII                                     Met Pro Val

50      60      70      80      90
*      *      *      *      *
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu

      100      110      120      130
      *      *      *      *
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys

      140      150      160      170
      *      *      *      *
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala

      180      190      200      210
      *      *      *      *
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser

      220      230      240      250
      *      *      *      *
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val

260      270      280      290      300
*      *      *      *      *
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val

      310      320      330      340
      *      *      *      *
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys

      350      360      370      380
      *      *      *      *
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly

      390      400      410      420      430
      *      *      *      *      *
TCA GGC GGA GGCCAAGTCGGCC ATCCCATATCAC GCGGCCGC GGATCC
Ser Gly Gly          SfiI                      NotI      BamHI

```

Figure 8B

```

1      10      20      30      40
*      *      *      *      *
AAGCTTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT
HindIII                               Met Pro Val

50      60      70      80      90
*      *      *      *      *
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu

100     110     120     130
*      *      *      *
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys

140     150     160     170
*      *      *      *
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala

180     190     200     210
*      *      *      *
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser

220     230     240     250
*      *      *      *
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val

260     270     280     290     300
*      *      *      *      *
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val

310     320     330     340
*      *      *      *
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys

350     360     370     380
*      *      *      *
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly

390     400     410     420     430
*      *      *      *      *
TCA GGC GGA G GGCCAAGTCGGCC ATCCCATATCAC GCGGCCGC GGATCC
Ser Gly Gly          SfiI                      NotI      BamHI

```


Figure 8C

```

1      10      20      30      40
*      *      *      *      *
AAGCTTTGCT AACATACTGC GTAATAAGGA GTCTTAATC ATG CCA GTT
HindIII                               Met Pro Val

50      60      70      80      90
*      *      *      *      *
CTT TTG GGT ATT CCG TTA TTA TTG CGT TTC CTC GGT TTC CTT
Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly Phe Leu

100     110     120     130
*      *      *      *
CTG GTA ACT TTG TTC GGC TAT CTG CTT ACT TTC CTT AAA AAG
Leu Val Thr Leu Phe Gly Tyr Leu Leu Thr Phe Leu Lys Lys

140     150     160     170
*      *      *      *
GGC TTC GGT AAG ATA GCT ATT GCT ATT TCA TTG TTT CTT GCT
Gly Phe Gly Lys Ile Ala Ile Ala Ile Ser Leu Phe Leu Ala

180     190     200     210
*      *      *      *
CTT ATT ATT GGG CTT AAC TCA ATT CTT GTG GGT TAT CTC TCT
Leu Ile Ile Gly Leu Asn Ser Ile Leu Val Gly Tyr Leu Ser

220     230     240     250
*      *      *      *
GAT ATT AGC GCA CAA TTA CCC TCT GAT TTT GTT CAG GGC GTT
Asp Ile Ser Ala Gln Leu Pro Ser Asp Phe Val Gln Gly Val

260     270     280     290     300
*      *      *      *      *
CAG TTA ATT CTC CCG TCT AAT GCG CTT CCC TGT TTT TAT GTT
Gln Leu Ile Leu Pro Ser Asn Ala Leu Pro Cys Phe Tyr Val

310     320     330     340
*      *      *      *
ATT CTC TCT GTA AAG GCT GCT ATT TTC ATT TTT GAC GTT AAA
Ile Leu Ser Val Lys Ala Ala Ile Phe Ile Phe Asp Val Lys

350     360     370     380
*      *      *      *
CAA AAA ATC GTT TCT TAT TTG GAT TGG GAT AAA GGT GGA GGC
Gln Lys Ile Val Ser Tyr Leu Asp Trp Asp Lys Gly Gly Gly

390     400     410     420     430
*      *      *      *      *
TCA GGC GGA TC GGCCAAGTCGGCC ATCCCATATCAC GCGGCCGC GGATCC
Ser Gly Gly          SfiI                      NotI      BamHI

```

Figure 9

```

1      10      20      30      40
*      *      *      *      *
GAATTCGG CTG GTW TCC TAC TGC AGT GGA AAA GCA ACG ATG
EcoRI      Leu Val Ser Tyr Cys Ser Gly Lys Ala Thr Met

      50      60      70      80
      *      *      *      *
CAG TGT GGT GAG AAT GAA AAG TAC GAT TCG TGC GGT AGC AAG
Gln Cys Gly Glu Asn Glu Lys Tyr Asp Ser Cys Gly Ser Lys

      90      100      110      120
      *      *      *      *
GAG TGC GAT AAG AAG TGC AAA TAT GAC GGA GTT GAG GAG GAA
Glu Cys Asp Lys Lys Cys Lys Tyr Asp Gly Val Glu Glu Glu

      130      140      150      160
      *      *      *      *
GAC GAC GAG GAA CCT AAT GTG CCA TGC CTA GTA CGT GTG TGT
Asp Asp Glu Glu Pro Asn Val Pro Cys Leu Val Arg Val Cys

      170      180      190      200      210
      *      *      *      *      *
CAT CAA GAT TGC GTA TGC GAA GAA GGA TTC TAT AGA AAC AAA
His Gln Asp Cys Val Cys Glu Glu Gly Phe Tyr Arg Asn Lys

      220      230      240      250
      *      *      *      *
GAT GAC AAA TGT GTA TCA GCA GAA GAC TGC GAA CTT GAC AAT
Asp Asp Lys Cys Val Ser Ala Glu Asp Cys Glu Leu Asp Asn

      260      270      280      290
      *      *      *      *
ATG GAC TTT ATA TAT CCC GGA ACT CGA AAC TGA ACGAAGGCTC
Met Asp Phe Ile Tyr Pro Gly Thr Arg Asn

      300      310      320      330      340
      *      *      *      *      *
CATTCTTGCT GCACAAGATC GATTGTCTCTCCCCTGCATCTCAGTAGTTTTGC

      350      360      370      380      390      400
      *      *      *      *      *
TACATTGTATATGGTAGCAAAAAATTAGCTTAGGGAGAATAAAATCTTTACCTAT

      410      420      430
      *      *      *
ATTTAATCAATGAAGTATTCTCTTTCT poly(A)

```

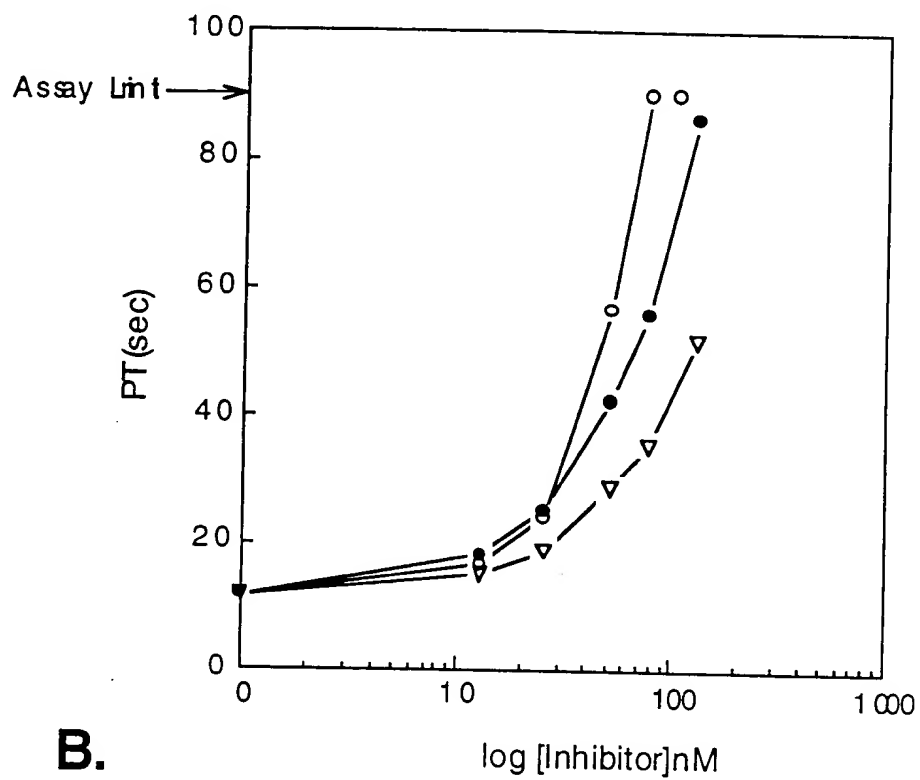
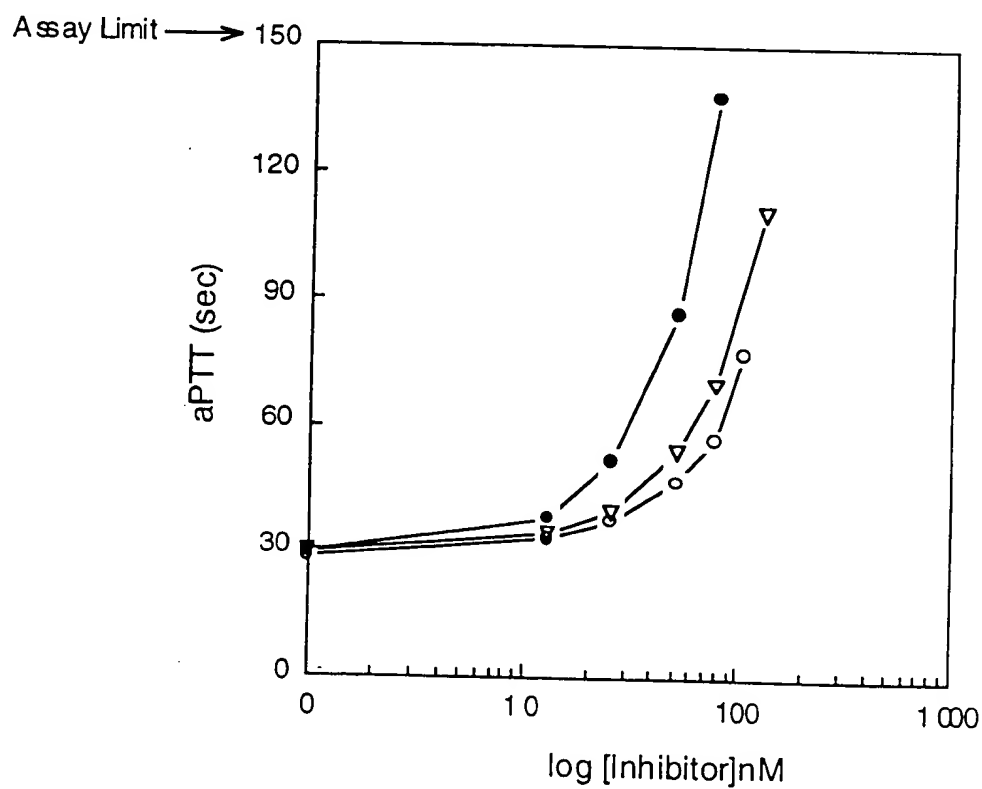
Figure 10**A.****B.**

Figure 11-1

NAP5	Met Lys Met Leu Tyr Ala Ile Ala Ile Met Phe Leu Leu Val
NAP6	Met Lys Met Leu Tyr Ala Ile Ala Ile Met Phe Leu Leu Val
NAPc2	Leu Val
AcenNAP5	Met Arg Thr Leu Tyr Leu Ile Ser Ile Trp Leu Phe Leu Ile
AcenNAP7	Met Ser Thr Leu Tyr Val Ile Ala Ile Cys Leu Leu Leu Val
AcenNAP4d1	Met Ala Val Leu Tyr Ser Val Ala Ile Ala Leu Leu Leu Val
AcenNAP4d2	
AduNAP4	
AduNAP7d1	Met Arg Met Leu Tyr Leu Val Pro Ile Trp Leu Leu Ile
AduNAP7d2	
HpoNAP5	Met Ile Arg Lys Leu Val Leu Leu Thr Ala Ile Val Thr

Figure 11-2

NAP5	Ser	Leu	Cys	Ser	Ala	Arg	Thr	Val	Arg	Lys	Ala	Tyr	Pro	Glu
NAP6	Ser	Leu	Cys	Ser	Thr	Arg	Thr	Val	Arg	Lys	Ala	Tyr	Pro	Glu
NAPc2	Ser	Tyr	Cys	Ser	Gly	---	---	---	---	Lys	Ala	Thr	Met	Gln
AcenAP5	Ser	Gln	Cys	Asn	Gly	---	---	---	---	Lys	Ala	Phe	Pro	Lys
AcenAP7	Ser	Gln	Cys	Asn	Gly	---	---	---	---	Arg	Thr	Val	Lys	Lys
AcenAP4d1	Ser	Gln	Cys	Ser	Gly	Lys	Pro	Asn	Asn	Val	Met	Thr	Asn	Ala
AcenAP4d2												Val	Pro	Ile
AdunAP4														Lys
AdunAP7d1	Ser	Leu	Cys	Ser	Gly	---	---	---	---	Lys	Ala	Ala	Lys	Lys
AdunAP7d2													Asp	Glu
HponAP5	Val	Val	Leu	Ser	Ala	---	---	---	---	---	---	---	Lys	Thr

Figure 11-3

NAP5	¹ Cys Gly Glu Asn Glu Trp Leu Asp Asp Cys ² Gly Thr Gln
NAP6	Cys Gly Glu Asn Glu Trp Leu Asp Val Cys Gly Thr Lys
NAPc2	Cys Gly Glu Asn Glu Lys Tyr Asp Ser Cys Gly Ser Lys
AcENAP5	Cys Asp Val Asn Glu Arg Phe Glu Val Cys Gly Asn Leu
AcENAP7	Cys Gly Lys Asn Glu Arg Tyr Asp Asp Cys Gly Asn Ala
AcENAP4d1	Cys Gly Leu Asn Glu Tyr Phe Ala Glu Cys Gly Asn Met
AcENAP4d2	Cys Gly Ser Asn Glu Arg Tyr Ser Asp Cys Gly Asn Asp
AduNAP4	Cys Pro Thr Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr
AduNAP7d1	Cys Gly Leu Asn Glu Arg Leu Asp --- Cys Gly Asn Leu
AduNAP7d2	Cys Gly Pro Asp Glu Trp Phe Asp Tyr Cys Gly Asn Tyr
HpoNAP5	Cys Gly Pro Asn Glu Glu Tyr Thr Glu Cys Gly Thr ---

Figure 11-4

NAP5	Lys	Pro	³ Cys	Glu	Ala	Lys	⁴ Cys	---	---	---	---	Asn	Glu	Glu
NAP6	Lys	Pro	Cys	Glu	Ala	Lys	Cys	---	---	---	---	Ser	Glu	Glu
NAPc2	Glu	---	Cys	ASP	Lys	Lys	Cys	Lys	Tyr	ASP	Gly	Val	Glu	Glu
AcENAP5	Lys	Glu	Cys	Glu	Leu	Lys	Cys	---	---	---	---	---	---	---
AcENAP7	Lys	ASP	Cys	Glu	Thr	Lys	Cys	---	---	---	Gly	---	---	---
AcENAP4d1	Lys	Glu	Cys	Glu	His	Arg	Cys	Asn	Glu	Glu	Glu	Asn	Glu	Glu
AcENAP4d2	Lys	Gln	Cys	Glu	Arg	Lys	Cys	Asn	Glu	ASP	ASP	Tyr	Glu	Lys
AduNAP4	Lys	His	Cys	Glu	Leu	Lys	Cys	ASP	Arg	Glu	Leu	Thr	Glu	Lys
AduNAP7d1	Lys	Gln	Cys	Glu	Pro	Lys	Cys	Ser	ASP	Leu	Glu	Ser	Glu	Glu
AduNAP7d2	Lys	Lys	Cys	Glu	Arg	Lys	Cys	Ser	Glu	Glu	Thr	Ser	Glu	Lys
HpoNAP5	---	Pro	Cys	Glu	Pro	Lys	Cys	---	---	---	---	---	---	---

Figure 11-5

NAP5	Pro	Pro	Glu	Glu	Glu	Asp	Pro	Ile	----	----	⁵ Cys	Arg	Ser	Arg
NAP6	----	----	Glu	Glu	Glu	Asp	Pro	Ile	----	----	Cys	Arg	Ser	Phe
NAPc2	----	Glu	Asp	Asp	Glu	Glu	Pro	Asn	Val	Pro	Cys	Leu	Val	Arg
AcenAP5	----	----	Asp	Glu	Asp	Pro	Lys	Ile	----	----	Cys	----	Ser	Arg
AcenAP7	----	----	Glu	Glu	Glu	----	Lys	----	Val	----	Cys	Arg	Ser	Arg
AcenAP4d1	Arg	----	Asp	Glu	Glu	----	Arg	Ile	Thr	Ala	Cys	Leu	Ile	Arg
AcenAP4d2	Gly	----	Asp	Glu	----	----	----	----	----	Ala	Cys	Arg	Ser	His
AdunAP4	----	----	Glu	Glu	----	----	Gln	----	----	Ala	Cys	Leu	Ser	Arg
AdunAP7d1	Tyr	----	Glu	Glu	Glu	Asp	Glu	Ser	Lys	----	Cys	Arg	Ser	Arg
AdunAP7d2	Asn	----	Glu	Glu	----	----	----	----	Ala	Cys	Leu	Ser	Arg	
HpoNAP5	----	----	Asn	Glu	Pro	Met	Pro	Asp	Ile	----	Cys	----	Thr	Leu

Figure 11-6

NAP5	Gly Cys ⁶ Leu Leu Pro Pro Ala Cys ⁷ Val Cys ⁸ Lys Asp
NAP6	Ser Cys Pro Gly Pro Ala Ala Cys Val Cys Glu Asp
NAPc2	Val Cys His Gln Asp - - - - Cys Val Cys Glu Glu
AcenAP5	Ala Cys Ile Arg Pro Pro Ala Cys Val Cys Asp Asp
AcenAP7	Glu Cys Thr Ser Pro Gly Ala Cys Val Cys Glu Gln
AcenAP4d1	Val Cys Phe Arg Pro Gly Ala Cys Val Cys Lys Asp
AcenAP4d2	Val Cys Glu Arg Pro Gly Ala Cys Val Cys Glu Asp
AduNAP4	Val Cys Glu Lys - - - Ser Ala Cys Val Cys Asn Asp
AduNAP7d1	Glu Cys Ser Arg Arg - - - Val Cys Val Cys Asp Glu
AduNAP7d2	Ala Cys Thr Gly Arg - - - Ala Cys Val Cys Lys Asp
HpoNAP5	Asn Cys Ile Val Asn - - - Val Cys Glu Cys Lys Pro

Figure 11-7

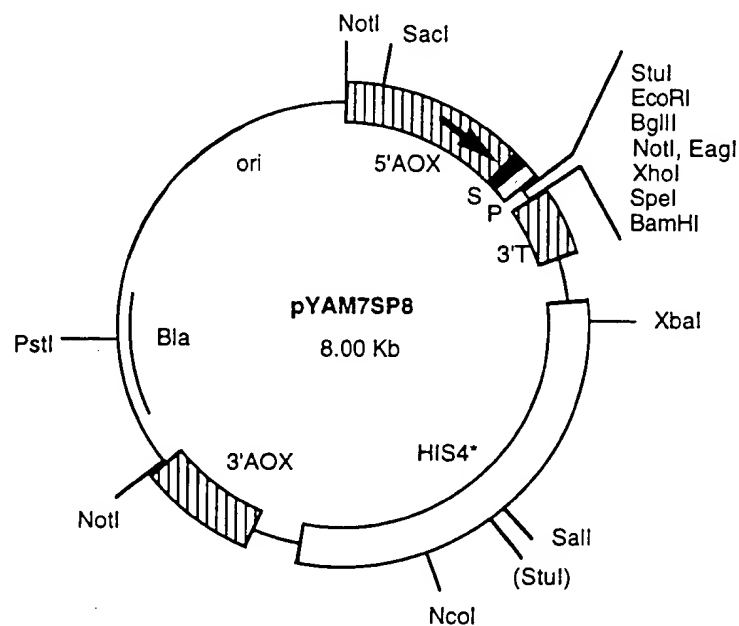
NAP5	Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys ⁹ Val Arg Glu
NAP6	Gly Phe Tyr Arg Asp Thr Val Ile Gly Asp Cys Val Lys Glu
NAPc2	Gly Phe Tyr Arg Asn Lys --- Asp Asp Lys Cys Val Ser Ala
AcenAP5	Gly Phe Tyr Arg Asp Lys Tyr --- Gly Phe Cys Val Glu Glu
AcenAP7	Gly Phe Tyr Arg Asp Pro Ala --- Gly Asp Cys Val Thr Asp
AcenAP4d1	Gly Phe Tyr Arg Asn Arg Thr --- Gly Ser Cys Val Glu Glu
AcenAP4d2	Gly Phe Tyr Arg Asn Lys Lys --- Gly Ser Cys Val Glu Ser
AdunAP4	Gly Leu Tyr Arg Asp Lys Phe --- Gly Asn Cys Val Glu Lys
AdunAP7d1	Gly Phe Tyr Arg Asn Lys Lys --- Gly Lys Cys Val Ala Lys
AdunAP7d2	Gly Leu Tyr Arg Asp Asp Phe --- Gly Asn Cys Val Pro His
HponAP5	Gly Phe Lys Arg Gly Pro Lys --- Gly --- Cys Val Ala Pro

Figure 11-8

NAP5	Glu Glu ---	¹⁰ Cys	Asp Gln His	---	---	Glu Ile Ile His
NAP6	Glu Glu ---	Cys	Asp Gln His	---	---	Glu Ile Ile His
NAPc2	Glu Asp ---	Cys	Glu ---	Leu Asp Asn Met Asp Phe Ile Tyr		
AcENAP5	Asp Glu ---	Cys	Asn Asp ---	---	---	Met Glu Ile Ile Thr
AcENAP7	Glu Glu ---	Cys	Asp Glu Trp Asn Asn Met Glu Ile Ile Thr			
AcENAP4d1	Asp Asp ---	Cys	Glu ---	Tyr Glu Asn Met Glu Phe Ile Thr		
AcENAP4d2	Asp Asp ---	Cys	Glu ---	Tyr Asp Asn Met Asp Phe Ile Thr		
AduNAP4	Asp Glu ---	Cys	Asn Asp ---	---	---	Met Glu Ile Ile Thr
AduNAP7d1	Asp Val ---	Cys	Glu Asp ---	Asp Asn Met Glu Ile Ile Thr		
AduNAP7d2	Asp Glu ---	Cys	Asn Asp ---	---	---	Met Glu Ile Ile Thr
HpoNAP5	Gly Pro Gly Cys Lys end					

Figure 11-9

NAP5	Val end
NAP6	Val end
NAPc2	Pro Gly Thr Arg Asn end
AcenAP5	Phe Pro Pro Glu Thr Lys end
AcenAP7	Met Pro Lys Gln end
AcenAP4d1	Phe Ala Pro Glu
AcenAP4d2	Phe Ala Pro Glu Thr Ser Arg end
AduNAP4	Phe Ala Pro Glu Thr Lys end
AduNAP7d1	Phe Pro Pro Glu
AduNAP7d2	Phe Pro Pro Glu Thr Lys His end
HponAP5	

Figure 12**A****B**

<----5'AOX1-----><-----PHO1 secretion signal (S)--

.....TTATTGAAACGATGTTCTCTCCAATTTTGTCTTGGAATTATTTTA

-----><-----Pro Sequence (P)-----

GCTACTTTGCAATCTGTCTTCGCCCAGCCAGTTATCTCCACTACCGTTGGTTCC

-----><-----Multi-Cloning Site (MCS)

GCTGCCGAGGGTTCTTTGGACAAGAGGCCTATCCGCGGAATTCAGATCTGAAT

StuI SacII EcoRI BglII

-----><-----3'T----->

GCGGCCGCTCGAGACTAGTGGATCCTTAGACA...

NotI XhoI SpeI BamHI

EagI

Figure 13 A-1 (AcanAP23)

```

      10      20      30      40
      *      *      *      *
  GAATTCCGCG GAATTCCGCT TGCTACTACT CAACG ATG AAG ACG CTC
  EcoRI                               Met Lys Thr Leu

  50      60      70      80
  *      *      *      *
  TAT ATT GTC GCT ATA TGC TCG CTC CTC ATT TCG CTG TGT ACT
  Tyr Ile Val Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr

  90      100      110      120      130
  *      *      *      *      *
  GGA AAA CCT TCG GAG AAA GAA TGT GGT CCC CAT GAA AGA CTC
  Gly Lys Pro Ser Glu Lys Glu Cys Gly Pro His Glu Arg Leu
      140      150      160      170
      *      *      *      *
  GAC TGT GGC AAC AAG AAG CCA TGC GAG CGC AAG TGC AAA ATA
  Asp Cys Gly Asn Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile
      180      190      200      210
      *      *      *      *
  GAG ACA AGT GAG GAG GAG GAT GAC TAC GAA GAG GGA ACC GAA
  Glu Thr Ser Glu Glu Glu Asp Asp Tyr Glu Glu Gly Thr Glu

  220      230      240      250
  *      *      *      *
  CGT TTT CGA TGC CTC TTA CGT GTG TGT GAT CAG CCT TAT GAA
  Arg Phe Arg Cys Leu Leu Arg Val Cys Asp Gln Pro Tyr Glu

  260      270      280      290
  *      *      *      *
  TGC ATA TGC GAT GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA
  Cys Ile Cys Asp Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu

  300      310      320      330      340
  *      *      *      *      *
  TGT GTG ACT GAT GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT
  Cys Val Thr Asp Asp Val Cys Gln Glu Asp Phe Met Glu Phe

      350      360      370      380
      *      *      *      *
  ATT ACT TTC GCA CCA TAA ACCCAATAAT GACCAATGAC TCCCATTCTT
  Ile Thr Phe Ala Pro

```

Figure 13 A-2

```
390          400          410          420          430
  *              *              *              *              *
  CGTGATCAGC GTCGGTGGTT GACAGTCTCC CCTACATCTT AGTAGTTTTG

440          450          460          470          480
  *              *              *              *              *
  CTTGATAATG TATACATAAA CTGTACTTTC TGAGATAGAA TAAAGCTCTC

490
  *
  AACTAC poly(A)
```

Figure 13 B-1 (AcaNAP24)

```

      10      20      30      40
      *      *      *      *
  GAATTCCGCG GAATTCCGCA ACG ATG AAG ACG CTC TAT ATT ATC
  EcoRI                      Met Lys Thr Leu Tyr Ile Ile

      50      60      70      80
      *      *      *      *
  GCT ATA TGC TCG CTC CTC ATT TCG TTG TGT ACT GGA AGA CCG
  Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro

      90     100     110     120
      *      *      *      *
  GAA AAA AAG TGC GGT CCC GGT GAA AGA CTC GCC TGT GGC AAT
  Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Ala Cys Gly Asn

 130     140     150     160     170
  *      *      *      *      *
  AAG AAG CCA TGC GAG CGC AAG TGC AAA ATA GAG ACA AGT GAG
  Lys Lys Pro Cys Glu Arg Lys Cys Lys Ile Glu Thr Ser Glu

      180     190     200     210
      *      *      *      *
  GAG GAG GAT GAC TAC CCA GAG GGA ACC GAA CGT TTT CGA TGC
  Glu Glu Asp Asp Tyr Pro Glu Gly Thr Glu Arg Phe Arg Cys

      220     230     240     250
      *      *      *      *
  CTC TTA CGT GTG TGT GAT CAG CCT TAT GAA TGC ATA TGC GAT
  Leu Leu Arg Val Cys Asp Gln Pro Tyr Glu Cys Ile Cys Asp

      260     270     280     290
      *      *      *      *
  GAT GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT
  Asp Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp

      300     310     320     330
      *      *      *      *
  GAT GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA
  Asp Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala

 340     350     360     370     380
  *      *      *      *      *
  CCA TAA ACCCAATAAT GACCACTGGC TCCCATTCTT CGTGACCAGC
  Pro

```


Figure 13 B-2

390	400	410	420	430
*	*	*	*	*
GTCGGTGGTT	GACAGTCTCC	CCTGCATCTT	AGTAGTTTTG	CTTGATAATG
440	450	460	470	
*	*	*	*	
TATCCATAAA	CAGTACTTTC	TGAGATAGAA	TAAAGCTCTC	AACT poly(A)

Figure 13 C (AcaNAP25)

```

      10      20      30      40
      *      *      *      *
  GAATTCGTA CTACTCAACG ATG AAG ACG CTC TAT ATT ATC GCT
  EcoRI                      Met Lys Thr Leu Tyr Ile Ile Ala

      50      60      70      80
      *      *      *      *
  ATA TGC TCG CTG CTC TTT TCA CTG TGT ACT GGA AGA CCG GAA
  Ile Cys Ser Leu Leu Phe Ser Leu Cys Thr Gly Arg Pro Glu

      90     100     110     120
      *      *      *      *
  AAA AAG TGC GGT CCC GGT GAA AGA CTC GAC TGT GCC AAC AAG
  Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn Lys

 130     140     150     160     170
  *      *      *      *      *
  AAG CCA TGC GAG CCC AAG TGC AAA ATA GAG ACA AGT GAG GAG
  Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu Glu

      180     190     200     210
      *      *      *      *
  GAG GAT GAC GAC GTA GAG GAT ACC GAT GTG AGA TGC CTC GTA
  Glu Asp Asp Asp Val Glu Asp Thr Asp Val Arg Cys Leu Val

      220     230     240     250
      *      *      *      *
  CGT GTG TGT GAA CGT CCT CTT AAA TGC ATA TGC AAG GAT GGA
  Arg Val Cys Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp Gly

      260     270     280     290
      *      *      *      *
  TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT GAT GTA
  Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp Asp Val

      300     310     320     330
      *      *      *      *
  TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA TAA
  Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro

 340     350     360     370     380
  *      *      *      *      *
  ACCCAATAAT GACCACTGGC TCCCATCTCTT CGTGATCAGC GTCGGTGGTT

 390     400     410     420     430
  *      *      *      *      *
  GACAGTCTCC CCTGCATCTT AGTTGCTTTG CTTGATAATC TATACATAAA

 440     450     460     470
  *      *      *      *
  CAGTACTTTC TGAGATAGAA TAAAGCTCTC AACT poly(A)

```

Figure 13 D-1 (AcaNAP31)

```

      10      20      30      40      50
      *      *      *      *      *
  GAATTCGGA CTTACTAGTA CTCAGCGAAT CAAATACGAC TTACTACTAC
  EcoRI
      60      70      80      90
      *      *      *      *
  TCAACG ATG AAG ACG CTC TCT GCT ATC CCT ATA ATG CTG CTC
    Met Lys Thr Leu Ser Ala Ile Pro Ile Met Leu Leu

     100     110     120     130
     *      *      *      *
  CTG GTA TCG CAA TGC AGT GGA AAA TCA CTG TGG GAT CAG AAG
  Leu Val Ser Gln Cys Ser Gly Lys Ser Leu Trp Asp Gln Lys

     140     150     160     170
     *      *      *      *
  TGT GGT GAG AAT GAA AGG CTC GAC TGT GGC AAT CAG AAG GAC
  Cys Gly Glu Asn Glu Arg Leu Asp Cys Gly Asn Gln Lys Asp

     180     190     200     210
     *      *      *      *
  TGT GAG CGC AAG TGC GAT GAT AAA AGA AGT GAA GAA GAA ATT
  Cys Glu Arg Lys Cys Asp Asp Lys Arg Ser Glu Glu Glu Ile

    220     230     240     250     260
    *      *      *      *      *
  ATG CAG GCA TGT CTC ACA CGT CAA TGT CTT CCT CCT GTT TGC
  Met Gln Ala Cys Leu Thr Arg Gln Cys Leu Pro Pro Val Cys

     270     280     290     300
     *      *      *      *
  GTA TGT GAA GAT GGA TTC TAC AGA AAT GAC AAC GAC CAA TGT
  Val Cys Glu Asp Gly Phe Tyr Arg Asn Asp Asn Asp Gln Cys

     310     320     330     340
     *      *      *      *
  GTT GAT GAA GAA GAA TGC AAT ATG GAG TTT ATT ACT TTC GCA
  Val Asp Glu Glu Glu Cys Asn Met Glu Phe Ile Thr Phe Ala

     350     360     370     380     390
     *      *      *      *      *
  CCA TGA AGCAAATGAC AGCCGATGGT TTGGA CTCTC GCTACAGATC
  Pro

     400     410     420     430     440
     *      *      *      *      *
  ACAGCTTTAC TGTTTCCTT GCATCATAGT AGTTTGTGCTA GATAGTGTAT

```

Figure 13 D-2

450	460	470	480
*	*	*	*
ATATTAGCAT	GATTTTCTGA	TAGGGAGAAT	AAAGCTTTCC
AATTTTC			
poly(A)			

Figure 13 E-1 (AcaNAP44)

```

      10      20      30      40
      *      *      *      *
  GAATTCGCG GAATTCGCA ACG ATG AAG ACG CTC TAT ATT ATC
  EcoRI                      Met Lys Thr Leu Tyr Ile Ile

      50      60      70      80
      *      *      *      *
  GCT ATA TGC TCG CTC CTC ATT TCG CTG TGT ACT GGA AGA CCG
  Ala Ile Cys Ser Leu Leu Ile Ser Leu Cys Thr Gly Arg Pro

      90     100     110     120
      *      *      *      *
  GAA AAA AAG TGC GGT CCC GGT GAA AGA CTC GAC TGT GCC AAC
  Glu Lys Lys Cys Gly Pro Gly Glu Arg Leu Asp Cys Ala Asn

 130     140     150     160     170
  *      *      *      *      *
  AAG AAG CCA TGC GAG CCC AAG TGC AAA ATA GAG ACA AGT GAG
  Lys Lys Pro Cys Glu Pro Lys Cys Lys Ile Glu Thr Ser Glu

      180     190     200     210
      *      *      *      *
  GAG GAG GAT GAC GAC GTA GAG GAA ACC GAT GTG AGA TGC CTC
  Glu Glu Asp Asp Asp Val Glu Glu Thr Asp Val Arg Cys Leu

      220     230     240     250
      *      *      *      *
  GTA CGT GTG TGT GAA CGG CCT CTT AAA TGC ATA TGC AAG GAT
  Val Arg Val Cys Glu Arg Pro Leu Lys Cys Ile Cys Lys Asp

      260     270     280     290
      *      *      *      *
  GGA TAC TAC AGA AAC AAG AAA GGC GAA TGT GTG ACT GAT GAT
  Gly Tyr Tyr Arg Asn Lys Lys Gly Glu Cys Val Thr Asp Asp

      300     310     320     330
      *      *      *      *
  GTA TGC CAG GAA GAC TTT ATG GAG TTT ATT ACT TTC GCA CCA
  Val Cys Gln Glu Asp Phe Met Glu Phe Ile Thr Phe Ala Pro

 340     350     360     370     380
  *      *      *      *      *
  TAA ACCCAATAAT GACCACTGGC TCCCATTCTT CGTGATCAGC

      390     400     410     420     430
      *      *      *      *      *
  GTCGGTGGTT GACAGTCTCC CCTGCATCTT AGTTGCTTTG CTTGATAATC

```

Figure 13 E-2

440	450	460	470
*	*	*	*
TATACATAAA	CAGTACTTTC	TGAGATAGAA	TAAAGCTCTC
AACTAC			

poly(A)

Figure 13 F-1 (AcaNAP45)

```

      10      20      30      40
      *      *      *      *
  GAATTCGGA AAA ATG CTG ATG CTC TAC CTT GTT CCT ATC TGG
  EcoRI      Met Leu Met Leu Tyr Leu Val Pro Ile Trp

      50      60      70      80
      *      *      *      *
  TTG CTA CTC ATT TCG CAA TGC AGT GGA AAA TCC GCG AAG AAA
  Leu Leu Leu Ile Ser Gln Cys Ser Gly Lys Ser Ala Lys Lys

      90      100      110      120
      *      *      *      *
  TGT GGT CTC AAT GAA AAA TTG GAC TGT GGC AAT CTG AAG GCA
  Cys Gly Leu Asn Glu Lys Leu Asp Cys Gly Asn Leu Lys Ala

      130      140      150      160
      *      *      *      *
  TGC GAG AAA AAG TGC AGC GAC TTG GAC AAT GAG GAG GAT TAT
  Cys Glu Lys Lys Cys Ser Asp Leu Asp Asn Glu Glu Asp Tyr

      170      180      190      200      210
      *      *      *      *      *
  AAG GAG GAA GAT GAG TCG AAA TGC CGA TCA CGT GAA TGT AGT
  Lys Glu Glu Asp Glu Ser Lys Cys Arg Ser Arg Glu Cys Ser

      220      230      240      250
      *      *      *      *
  CGT CGT GTT TGT GTA TGC GAT GAA GGA TTC TAC AGA AAC AAG
  Arg Arg Val Cys Val Cys Asp Glu Gly Phe Tyr Arg Asn Lys

      260      270      280      290
      *      *      *      *
  AAG GGC CAA TGT GTG ACA AGA GAT GAT TGC GAG TAT GAC AAT
  Lys Gly Gln Cys Val Thr Arg Asp Asp Cys Glu Tyr Asp Asn

      300      310      320      330
      *      *      *      *
  ATG GAG ATT ATC ACT TTT CCA CCA GAA GAT AAA TGT GGT CCC
  Met Glu Ile Ile Thr Phe Pro Pro Glu Asp Lys Cys Gly Pro

      340      350      360      370
      *      *      *      *
  GAT GAA TGG TTC GAC TGG TGT GGA ACT TAC AAG CAG TGT GAG
  Asp Glu Trp Phe Asp Trp Cys Gly Thr Tyr Lys Gln Cys Glu

      380      390      400      410      420
      *      *      *      *      *
  CGC AAG TGC AAT AAG GAG CTA AGT GAG AAA GAT GAA GAG GCA
  Arg Lys Cys Asn Lys Glu Leu Ser Glu Lys Asp Glu Glu Ala

```



100

Figure 13 G-1 (AcaNAP47)

```

      10      20      30      40
      *      *      *      *
  GAATTCGCG GAATTCGGT TGGCGGCAGA AAA ATG CTG ATG CTC
  EcoRI                               Met Leu Met Leu

      50      60      70      80
      *      *      *      *
  TAC CTT GTT CCT ATC TGG TTC CTG CTC ATT TCG CAA TGC AGT
  Tyr Leu Val Pro Ile Trp Phe Leu Leu Ile Ser Gln Cys Ser

      90      100      110      120
      *      *      *      *
  GGA AAA TCC GCG AAG AAA TGT GGC CTC AAT GAA AAA TTG GAC
  Gly Lys Ser Ala Lys Lys Cys Gly Leu Asn Glu Lys Leu Asp

130      140      150      160      170
  *      *      *      *      *
  TGT GGC AAT CTG AAG GCA TGC GAG AAA AAG TGC AGC GAC TTG
  Cys Gly Asn Leu Lys Ala Cys Glu Lys Lys Cys Ser Asp Leu

      180      190      200      210
      *      *      *      *
  GAC AAT GAG GAG GAT TAT GGG GAG GAA GAT GAG TCG AAA TGC
  Asp Asn Glu Glu Asp Tyr Gly Glu Glu Asp Glu Ser Lys Cys

      220      230      240      250
      *      *      *      *
  CGA TCA CGT GAA TGT ATT GGT CGT GTT TGC GTA TGC GAT GAA
  Arg Ser Arg Glu Cys Ile Gly Arg Val Cys Val Cys Asp Glu

      260      270      280      290
      *      *      *      *
  GGA TTC TAC AGA AAC AAG AAG GGC CAA TGT GTG ACA AGA GAC
  Gly Phe Tyr Arg Asn Lys Lys Gly Gln Cys Val Thr Arg Asp

      300      310      320      330
      *      *      *      *
  GAT TGC GAG TAT GAC AAT ATG GAG ATT ATC ACT TTT CCA CCA
  Asp Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro

340      350      360      370      380
  *      *      *      *      *
  GAA GAT AAA TGT GGT CCC GAT GAA TGG TTC GAC TGG TGT GGA
  Glu Asp Lys Cys Gly Pro Asp Glu Trp Phe Asp Trp Cys Gly

      390      400      410      420
      *      *      *      *
  ACT TAC AAG CAG TGT GAG CGC AAG TGC AGT GAG GAG CTA AGT
  Thr Tyr Lys Gln Cys Glu Arg Lys Cys Ser Glu Glu Leu Ser

```

Figure 13 G-2

430	440	450	460
*	*	*	*
GAG AAA AAT GAG GAG GCA TGC CTC TCA CGT GCT TGT ACT GGT			
Glu Lys Asn Glu Glu Ala Cys Leu Ser Arg Ala Cys Thr Gly			
470	480	490	500
*	*	*	*
CGT GCT TGC GTT TGC AAC GAC GGA TTG TAT AGA GAC GAT TTT			
Arg Ala Cys Val Cys Asn Asp Gly Leu Tyr Arg Asp Asp Phe			
510	520	530	540
*	*	*	*
GGC AAT TGT GTT GAG AAA GAC GAA TGT AAC GAT ATG GAG ATT			
Gly Asn Cys Val Glu Lys Asp Glu Cys Asn Asp Met Glu Ile			
550	560	570	580
*	*	*	*
ATC ACT TTT CCA CCG GAA ACC AAA CAC TGA CCAAAGGCTC			
Ile Thr Phe Pro Pro Glu Thr Lys His			
590	600	610	620
*	*	*	*
TAGCTCTCGC TACATAACGT CAGTGCTTGA ATTGTCCCTT TACGTGTTAG			
640	650	660	670
*	*	*	*
TAATTTTGAC TAACTCTGTG TATTTGAGCA TTGTCTACTA ATGGTGAAAA			
690	700		
*	*		
TGAAGCTTTT CAATGACT poly(A)			

Figure 13 H-1 (AcaNAP48)

```

      10      20      30      40
      *      *      *      *
  GAATTCGTA CGACCTACTA CTAACAACG ATG AAG GCG CTC TAT
  EcoRI                      Met Lys Ala Leu Tyr

      50      60      70      80
      *      *      *      *
  GTT ATC TCT ATA ACG TTG CTC CTG GTA TGG CAA TGC AGT GCA
  Val Ile Ser Ile Thr Leu Leu Val Trp Gln Cys Ser Ala

      90      100      110      120
      *      *      *      *
  AGA ACA GCG AGG AAA CCC CCA ACG TGT GGT GAA AAT GAA AGG
  Arg Thr Ala Arg Lys Pro Pro Thr Cys Gly Glu Asn Glu Arg

130      140      150      160      170
  *      *      *      *      *
  GTC GAA TGG TGT GGC AAG CAG TGC GAG ATC ACA TGT GAC GAC
  Val Glu Trp Cys Gly Lys Gln Cys Glu Ile Thr Cys Asp Asp

      180      190      200      210
      *      *      *      *
  CCA GAT AAG ATA TGC CGC TCA CTC GCT TGT CCT GGT CCT CCT
  Pro Asp Lys Ile Cys Arg Ser Leu Ala Cys Pro Gly Pro Pro

      220      230      240      250
      *      *      *      *
  GCT TGC GTA TGC GAC GAC GGA TAC TAC AGA GAC ACG AAC GTT
  Ala Cys Val Cys Asp Asp Gly Tyr Tyr Arg Asp Thr Asn Val

      260      270      280      290
      *      *      *      *
  GGC TTG TGT GTA CAA TAT GAC GAA TGC AAC GAT ATG GAT ATT
  Gly Leu Cys Val Gln Tyr Asp Glu Cys Asn Asp Met Asp Ile

300      310      320      330      340
  *      *      *      *      *
  ATT ATG GTT TCA TAG GGTTGACTGA AGAATCGAAC AACCGGTGCA
  Ile Met Val Ser

      350      360      370      380      390
      *      *      *      *      *
  CAACTTCTAT GCTTGACTAT CTCTCTTGCA TCATGCAAGT TTAGCTAGAT

      400      410      420      430      440
      *      *      *      *      *
  AGTGTATATA TTAGCAAGAC CCCTTGGGGA GAATGAAGCT TCCCAACTAT

      450      460      470      480      490
      *      *      *      *      *
  ATTAAATCAA TAACGTTTTC GCTTCATGTA CACGTGCTCA GCACATTCAT

```

Figure 13 H-2

500	510	520	
*	*	*	
ATCCACTCCT CACTCCAT GAAAGCAGTG AAATGTT poly(A)			

Figure 14

```

      10      20      30      40
      *      *      *      *
GCC AAC TCT TCG AAC ATG ATT CGA GGC CTC GTT CTT CTT TCT CTC CTG
      Met Ile Arg Gly Leu Val Leu Leu Ser Leu Leu>

      50      60      70      80      90
      *      *      *      *      *
TTT TGC GTC ACT TTT GCA GCG AAG AGA GAT TGT CCA GCA AAT GAG GAA
Phe Cys Val Thr Phe Ala Ala Lys Arg Asp Cys Pro Ala Asn Glu Glu>

      100      110      120      130      140
      *      *      *      *      *
TGG AGG GAA TGT GGC ACT CCA TGT GAA CCA AAA TGC AAT CAA CCG ATG
Trp Arg Glu Cys Gly Thr Pro Cys Glu Pro Lys Cys Asn Gln Pro Met>

      150      160      170      180      190
      *      *      *      *      *
CCA GAT ATA TGT ACT ATG AAT TGT ATC GTC GAT GTG TGT CAA TGC AAG
Pro Asp Ile Cys Thr Met Asn Cys Ile Val Asp Val Cys Gln Cys Lys>

      200      210      220      230      240
      *      *      *      *      *
GAG GGA TAC AAG CGT CAT GAA ACG AAG GGA TGC TTA AAG GAA GGA TCA
Glu Gly Tyr Lys Arg His Glu Thr Lys Gly Cys Leu Lys Glu Gly Ser>

      250      260      270      280
      *      *      *      *
GCT GAT TGT AAA TAA GTT ATC AGA ACG CTC GTT TTG TCT TAC ATT AGA
Ala Asp Cys Lys ***

      290      300      310      320      330
      *      *      *      *      *
TGG GTG AGC TGA TGT ATC TGT CAG ATA AAC TCT TTC TTC TAA AAA AAA

      340      350      360
      *      *      *
AAA AAA AAA AAA AAA AAA AAA A

```

FIGURE 15

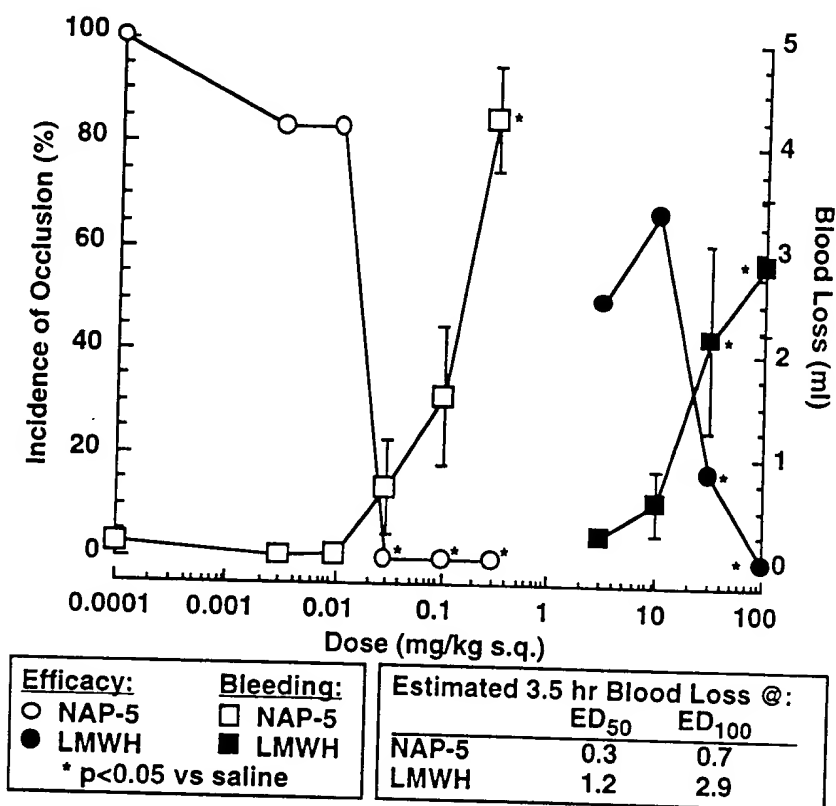


FIGURE 16

[illegible]

Figure 17

Lys Pro Asn Asn Val Met Thr Asn Ala **Cys** Gly Leu Asn Glu
 1 5 10
 Tyr Phe Ala Glu **Cys** Gly Asn Met Lys Glu **Cys** Glu His Arg
 15 20 25
Cys Asn Glu Glu Glu Asn Glu Glu Arg Asp Glu Glu Arg Ile
 30 35 40
 Thr Ala **Cys** Leu Ile Arg Val **Cys** Phe Arg Pro Gly Ala **Cys**
 45 50 55
 Val **Cys** Lys Asp Gly Phe Tyr Arg Asn Arg Thr Gly Ser **Cys**
 60 65 70
 Val Glu Glu Asp Asp **Cys** Glu Tyr Glu Asn Met Glu Phe Ile
 75 80
 Thr Phe Ala Pro Glu Val Pro Ile **Cys** Gly Ser Asn Glu Arg
 85 90 95
 Tyr Ser Asp **Cys** Gly Asn Asp Lys Gln **Cys** Glu Arg Lys **Cys**
 100 105 110
 Asn Glu Asp Asp Tyr Glu Lys Gly Asp Glu Ala **Cys** Arg Ser
 115 120 125
 His Val **Cys** Glu Arg Pro Gly Ala **Cys** Val **Cys** Glu Asp Gly
 130 135 140
 Phe Tyr Arg Asn Lys Lys Gly Ser **Cys** Val Glu Ser Asp Asp
 145 150
Cys Glu Tyr Asp Asn Met Asp Phe Ile Thr Phe Ala Pro Glu
 155 160 165
 Thr Ser Arg
 170

Figure 18

Lys Ser Ala Lys Lys **Cys** Gly Leu Asn Glu Lys Leu Asp **Cys**
 1 5 10
 Gly Asn Leu Lys Ala **Cys** Glu Lys Lys **Cys** Ser Asp Leu Asp
 15 20 25
 Asn Glu Glu Asp Tyr Lys Glu Glu Asp Glu Ser Lys **Cys** Arg
 30 35 40
 Ser Arg Glu **Cys** Ser Arg Arg Val **Cys** Val **Cys** Asp Glu Gly
 45 50 55
 Phe Tyr Arg Asn Lys Lys Gly Gln **Cys** Val Thr Arg Asp Asp
 60 65 70
Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu
 75 80
 Asp Lys **Cys** Gly Pro Asp Glu Trp Phe Asp Trp **Cys** Gly Thr
 85 90 95
 Tyr Lys Gln **Cys** Glu Arg Lys **Cys** Asn Lys Glu Leu Ser Glu
 100 105 110
 Lys Asp Glu Glu Ala **Cys** Leu Ser Arg Ala **Cys** Thr Gly Arg
 115 120 125
 Ala **Cys** Val **Cys** Asn Asp Gly Leu Tyr Arg Asp Asp Phe Gly
 130 135 140
 Asn **Cys** Val Glu Lys Asp Glu **Cys** Asn Asp Met Glu Ile Ile
 145 150
 Thr Phe Pro Pro Glu Thr Lys His
 155 160

Figure 19

Lys Ser Ala Lys Lys **Cys** Gly Leu Asn Glu Lys Leu Asp **Cys**
 1 5 10
 Gly Asn Leu Lys Ala **Cys** Glu Lys Lys **Cys** Ser Asp Leu Asp
 15 20 25
 Asn Glu Glu Asp Tyr Gly Glu Glu Asp Glu Ser Lys **Cys** Arg
 30 35 40
 Ser Arg Glu **Cys** Ile Gly Arg Val **Cys** Val **Cys** Asp Glu Gly
 45 50 55
 Phe Tyr Arg Asn Lys Lys Gly Gln **Cys** Val Thr Arg Asp Asp
 60 65 70
Cys Glu Tyr Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu
 75 80
 Asp Lys **Cys** Gly Pro Asp Glu Trp Phe Asp Trp **Cys** Gly Thr
 85 90 95
 Tyr Lys Gln **Cys** Glu Arg Lys **Cys** Ser Glu Glu Leu Ser Glu
 100 105 110
 Lys Asn Glu Glu Ala **Cys** Leu Ser Arg Ala **Cys** Thr Gly Arg
 115 120 125
 Ala **Cys** Val **Cys** Asn Asp Gly Leu Tyr Arg Asp Asp Phe Gly
 130 135 140
 Asn **Cys** Val Glu Lys Asp Glu **Cys** Asn Asp Met Glu Ile Ile
 145 150
 Thr Phe Pro Pro Glu Thr Lys His
 155 160

Figure 20

Lys Ala Ala Lys Lys **Cys** Gly Leu Asn Glu Arg Leu Asp **Cys**
 1 5 10
 Gly Asn Leu Lys Gln **Cys** Glu Pro Lys **Cys** Ser Asp Leu Glu
 15 20 25
 Ser Glu Glu Tyr Glu Glu Glu Asp Glu Ser Lys **Cys** Arg Ser
 30 35 40
 Arg Glu **Cys** Ser Arg Arg Val **Cys** Val **Cys** Asp Glu Gly Phe
 45 50 55
 Tyr Arg Asn Lys Lys Gly Lys **Cys** Val Ala Lys Asp Val **Cys**
 60 65 70
 Glu Asp Asp Asn Met Glu Ile Ile Thr Phe Pro Pro Glu Asp
 75 80
 Glu **Cys** Gly Pro Asp Glu Trp Phe Asp Tyr **Cys** Gly Asn Tyr
 85 90 95
 Lys Lys **Cys** Glu Arg Lys **Cys** Ser Glu Glu Thr Ser Glu Lys
 100 105 110
 Asn Glu Glu Ala **Cys** Leu Ser Arg Ala **Cys** Thr Gly Arg Ala
 115 120 125
Cys Val **Cys** Lys Asp Gly Leu Tyr Arg Asp Asp Phe Gly Asn
 130 135 140
Cys Val Pro His Asp Glu **Cys** Asn Asp Met Glu Ile Ile Thr
 145 150
 Phe Pro Pro Glu Thr Lys His
 155 160